



SEQUENCE LISTING

<110> MORI, SATOSHI
HIGUCHI, KYOKO
SUZUKI, KAZUYA
NISHIZAWA, NAOKO
NAKANISHI, HIROMI

<120> NICOTIANAMINE SYNTHASE AND GENE ENCODING THE SAME

<130> 71526-55107

<140> 09/674,337
<141> 2001-07-26

<150> PCT/JP99/02305
<151> 1999-04-30

<150> JP 10-137685
<151> 1998-04-30

<160> 37

<170> PatentIn Ver. 3.2

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<212> PRT
<213> Hordeum vulgare

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35 40 45

Ser Pro Val Asp Val Thr Lys Leu Ser Pro Glu His Gln Arg Met Arg
50 55 60

Glu Ala Leu Ile Arg Leu Cys Ser Ala Ala Glu Gly Lys Leu Glu Ala
65 70 75 80

His Tyr Ala Asp Leu Leu Ala Thr Phe Asp Asn Pro Leu Asp His Leu
85 90 95

Gly Leu Phe Pro Tyr Tyr Ser Asn Tyr Val Asn Leu Ser Arg Leu Glu
100 105 110

Tyr Glu Leu Leu Ala Arg His Val Pro Gly Ile Ala Pro Ala Arg Val
115 120 125

Ala Phe Val Gly Ser Gly Pro Leu Pro Phe Ser Ser Leu Val Leu Ala
130 135 140

Ala His His Leu Pro Glu Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly
 145 150 155 160

Ala Ala Asn Glu Arg Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly
 165 170 175

Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr
 180 185 190

Gln Glu Leu Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly
 195 200 205

Met Ala Ala Glu Glu Lys Ala Lys Val Ile Ala His Leu Gly Ala His
 210 215 220

Met Val Glu Gly Ala Ser Leu Val Val Arg Ser Ala Arg Pro Arg Gly
 225 230 235 240

Phe Leu Tyr Pro Ile Val Asp Pro Glu Asp Ile Arg Arg Gly Gly Phe
 245 250 255

Glu Val Leu Ala Val His His Pro Glu Gly Glu Val Ile Asn Ser Val
 260 265 270

Ile Val Ala Arg Lys Ala Val Glu Ala Gln Leu Ser Gly Pro Gln Asn
 275 280 285

Gly Asp Ala His Ala Arg Gly Ala Val Pro Leu Val Ser Pro Pro Cys
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Asn Phe Ser Thr Lys Met Glu Ala Ser Ala Leu Glu Lys Ser Glu Glu
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Leu Thr Ala Lys Glu Leu Ala Phe
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 <213> Hordeum vulgare

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 Asp Ala Gln Asn Lys Glu Val Ala Ala Leu Ile Glu Lys Ile Ala Gly
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atc cag gcc gcc atc gcc gag ctg ccg tcg ctg agc ccg tcc ccc gag 153
 Ile Gln Ala Ala Ile Ala Glu Leu Pro Ser Leu Ser Pro Ser Pro Glu
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gtc gac agg ctc ttc acc gac ctc gtc acg gcc tgc gtc ccg ccg agc	201
Val Asp Arg Leu Phe Thr Asp Leu Val Thr Ala Cys Val Pro Pro Ser	
35 40 45	
ccc gtc gac gtg acg aag ctc agc ccg gag cac cag agg atg cg ^g gag	249
Pro Val Asp Val Thr Lys Leu Ser Pro Glu His Gln Arg Met Arg Glu	
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gct ctc atc cgc ttg tgc tcc gcc gag ggg aag ctc gag g ^c gac	297
Ala Leu Ile Arg Leu Cys Ser Ala Ala Glu Gly Lys Leu Glu Ala His	
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Tyr Ala Asp Leu Leu Ala Thr Phe Asp Asn Pro Leu Asp His Leu Gly	
85 90 95	
ctc ttc ccg tac tac agc aac tac gtc aac ctc agc agg ctg gag tac	393
Leu Phe Pro Tyr Tyr Ser Asn Tyr Val Asn Leu Ser Arg Leu Glu Tyr	
100 105 110	
gag ctc ctg g ^c cgc cac gtg ccg ggc atc g ^c ccg g ^c g ^c g ^c g ^c g ^c	441
Glu Leu Leu Ala Arg His Val Pro Gly Ile Ala Pro Ala Arg Val Ala	
115 120 125	
ttc gtc ggc tcc ggc ccg ctg ccg ttc agc tcg ctc gtc ctc gcc g ^c	489
Phe Val Gly Ser Gly Pro Leu Pro Phe Ser Ser Leu Val Leu Ala Ala	
130 135 140 145	
cac cac ctg ccc gag acc cag ttc gac aac tac gac ctg tcg ggc g ^c	537
His His Leu Pro Glu Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly Ala	
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gcc aac gag cgc gcc agg aag ctg ttc ggc g ^c acg g ^c g ^c g ^c g ^c g ^c	585
Ala Asn Glu Arg Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly Val	
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ggc g ^c cgt atg tcg ttc cac acg g ^c gac gtc gcc gac ctc acc cag	633
Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Gln	
180 185 190	
gag ctc ggc gcc tac gac gtg gtc ttc ctc gcc g ^c ctc gtc ggc atg	681
Glu Leu Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met	
195 200 205	
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Ala Ala Glu Glu Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met	
210 215 220 225	
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Val Glu Gly Ala Ser Leu Val Val Arg Ser Ala Arg Pro Arg Gly Phe	
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ctt tac ccc att gtc gac ccg gag gac atc agg cgg ggt ggg ttc gag	825
Leu Tyr Pro Ile Val Asp Pro Glu Asp Ile Arg Arg Gly Gly Phe Glu	
245 250 255	

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Val Leu Ala Val His His Pro Glu Gly Glu Val Ile Asn Ser Val Ile	
260 265 270	
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Val Ala Arg Lys Ala Val Glu Ala Gln Leu Ser Gly Pro Gln Asn Gly	
275 280 285	
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Asp Ala His Ala Arg Gly Ala Val Pro Leu Val Ser Pro Pro Cys Asn	
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Phe Ser Thr Lys Met Glu Ala Ser Ala Leu Glu Lys Ser Glu Glu Leu	
310 315 320	
acc gcc aaa gag ctg gcc ttt tga ttgaagagtg cgcgtggtca ttctgtcgcc	1071
Thr Ala Lys Glu Leu Ala Phe	
325	
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 <212> PRT
 <213> Hordeum vulgare

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Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala Cys Val Pro	
35 40 45	
Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala Gln Glu Met	
50 55 60	
Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu Glu	
65 70 75 80	
Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp Lys Pro Leu Asp His	
85 90 95	
Leu Gly Met Phe Pro Tyr Tyr Asn Asn Tyr Ile Asn Leu Ser Lys Leu	
100 105 110	

Glu Tyr Glu Leu Leu Ala Arg Tyr Val Pro Gly Gly Tyr Arg Pro Ala
 115 120 125
 Arg Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Phe Val
 130 135 140
 Leu Ala Ala Arg His Leu Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu
 145 150 155 160
 Cys Gly Ala Ala Asn Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Arg
 165 170 175
 Asp Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu
 180 185 190
 Ala Gly Glu Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val
 195 200 205
 Gly Met Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala
 210 215 220
 His Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala
 225 230 235 240
 Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly
 245 250 255
 Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn
 260 265 270
 Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Val His Ala Asp Gly Leu
 275 280 285
 Gly Ser Gly Arg Gly Ala Gly Gln Tyr Ala Arg Gly Thr Val Pro
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 325 330 335

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 <212> DNA
 <213> Hordeum vulgare

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 ccaccgagtc cagtggacgt gaccaagctc gggccggagg cgcaggagat gcgggaggggc 240
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 aacctcagca agctcgagta cgagcttcg gcccgtacg tgcctggcggtt cttatcgcccg 420
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<210> 5
 <211> 335
 <212> PRT
 <213> Hordeum vulgare

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 Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala Cys Val
 35 40 45
 Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala Gln Glu
 50 55 60
 Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu
 65 70 75 80
 Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp Asn Pro Leu Asp
 85 90 95
 His Leu Gly Ile Phe Pro Tyr Tyr Ser Asn Tyr Ile Asn Leu Ser Lys
 100 105 110
 Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val Arg Arg His Arg Pro Ala
 115 120 125
 Arg Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Phe Val
 130 135 140
 Leu Ala Ala Arg His Leu Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu
 145 150 155 160
 Cys Gly Ala Ala Asn Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Thr
 165 170 175
 Asp Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu
 180 185 190

Ala Ser Glu Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val
 195 200 205

Gly Met Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala
 210 215 220

His Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala
 225 230 235 240

Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly
 245 250 255

Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn
 260 265 270

Ser Val Ile Ile Ala Gln Lys Ser Lys Glu Val His Ala Asp Gly Leu
 275 280 285

Gly Ser Ala Arg Gly Ala Gly Arg Gln Tyr Ala Arg Gly Thr Val Pro
 290 295 300

Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val Thr
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Gln Asn His Lys Arg Asp Glu Phe Ala Asn Ala Glu Val Ala Phe
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<211> 1314

<212> DNA

<213> Hordeum vulgare

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 tteccccgag ccccgtggac gtgaccaagg tcggccccga ggcgcaggag atgcgggagg 240
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 agggtttaca cggaaatgtc tttacacctt gtacgtgtaa gtgttgcacaa cgatgaattt 1260
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 <212> PRT
 <213> Hordeum vulgare

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 Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro Ser Pro
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 Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys Val Pro Pro
 35 40 45
 Ser Pro Val Asp Val Thr Lys Leu Ala Pro Glu Ala Gln Ala Met Arg
 50 55 60
 Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu Glu Ala
 65 70 75 80
 His Tyr Ser Asp Met Leu Ala Ala Phe Asp Asn Pro Leu Asp His Leu
 85 90 95
 Gly Val Phe Pro Tyr Tyr Ser Asn Tyr Ile Asn Leu Ser Lys Leu Glu
 100 105 110
 Tyr Glu Leu Leu Ala Arg Tyr Val Pro Gly Arg His Arg Pro Ala Arg
 115 120 125
 Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Tyr Val Leu
 130 135 140
 Ala Ala Arg His Leu Pro Asp Thr Val Phe Asp Asn Tyr Asp Leu Cys
 145 150 155 160
 Gly Ala Ala Asn Asp Arg Ala Thr Arg Leu Phe Arg Ala Asp Lys Asp
 165 170 175
 Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr
 180 185 190
 Asp Glu Leu Ala Thr Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly
 195 200 205
 Met Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His
 210 215 220
 Met Ala Asp Gly Ala Ala Leu Val Ala Arg His Gly Ala Arg Gly Phe
 225 230 235 240
 Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly Phe Glu
 245 250 255
 Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn Ser Val Ile
 260 265 270

Ile Ala Gln Lys Ser Asn Asp Val His Glu Tyr Gly Leu Gly Ser Gly
 275 280 285

Arg Gly Gly Arg Tyr Ala Arg Gly Thr Val Val Pro Val Val Ser Pro
 290 295 300

Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val Thr Gln Lys Arg Glu
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Glu Phe Ala Asn Ala Glu Val Ala Phe
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<210> 8

<211> 1249

<212> DNA

<213> Hordeum vulgare

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<211> 282

<212> PRT

<213> Hordeum vulgare

<400> 9

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Gln Val Asp Ala Leu Phe Thr Glu Leu Val Ala Ala Cys Val Pro Ser
 35 40 45

Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala Gln Glu Met Arg
 50 55 60

Gln Asp Leu Ile Arg Leu Cys Ser Ala Ala Glu Gly Leu Leu Glu Ala
 65 70 75 80

His Tyr Ser Asp Met Leu Thr Ala Leu Asp Ser Pro Leu Asp His Leu
 85 90 95

Gly Arg Phe Pro Tyr Phe Asp Asn Tyr Val Asn Leu Ser Lys Leu Glu
 100 105 110

His Asp Leu Leu Ala Gly His Val Ala Ala Pro Ala Arg Val Ala Phe
 115 120 125

Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Leu Phe Leu Ala Thr Tyr
 130 135 140

His Leu Pro Asp Thr Arg Phe Asp Asn Tyr Asp Arg Cys Ser Val Ala
 145 150 155 160

Asn Gly Arg Ala Met Lys Leu Val Gly Ala Ala Asp Glu Gly Val Arg
 165 170 175

Ser Arg Met Ala Phe His Thr Ala Glu Val Thr Asp Leu Thr Ala Glu
 180 185 190

Leu Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Thr
 195 200 205

Ser Lys Glu Lys Ala Asp Ala Ile Ala His Leu Gly Lys His Met Ala
 210 215 220

Asp Gly Ala Val Leu Val Arg Glu Ala Leu His Gly Ala Arg Ala Phe
 225 230 235 240

Leu Tyr Pro Val Val Glu Leu Asp Asp Val Gly Arg Gly Gly Phe Gln
 245 250 255

Val Leu Ala Val His His Pro Ala Gly Asp Glu Val Phe Asn Ser Phe
 260 265 270

Ile Val Ala Arg Lys Val Lys Met Ser Ala
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 <212> DNA
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 35 40 45
 Ser Pro Val Asp Val Thr Lys Leu Gly Ser Glu Ala Gln Glu Met Arg
 50 55 60
 Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu Glu Ala
 65 70 75 80
 His Tyr Ser Asp Met Leu Ala Ala Phe Asp Asn Pro Leu Asp His Leu
 85 90 95
 Gly Met Phe Pro Tyr Tyr Ser Asn Tyr Ile Asn Leu Ser Lys Leu Glu
 100 105 110
 Tyr Glu Leu Leu Ala Arg Tyr Val Pro Gly Gly Ile Ala Arg Pro Ala
 115 120 125
 Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Tyr Val Leu
 130 135 140
 Ala Ala Arg His Leu Pro Asp Ala Met Phe Asp Asn Tyr Asp Leu Cys
 145 150 155 160
 Ser Ala Ala Asn Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Lys Asp
 165 170 175
 Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr
 180 185 190
 Arg Glu Leu Ala Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly
 195 200 205

Met Ala Ala Glu Asp Lys Ala Lys Val Ile Pro His Leu Gly Ala His
 210 215 220

Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala Gln Ala Arg Gly
 225 230 235 240

Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly Phe
 245 250 255

Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn Ser Val
 260 265 270

Ile Ile Ala His Lys Ser Lys Asp Val His Ala Asn Glu Arg Pro Asn
 275 280 285

Gly Arg Gly Gly Gln Tyr Arg Gly Ala Val Pro Val Val Ser Pro Pro
 290 295 300

Cys Arg Phe Gly Glu Met Val Ala Asp Val Thr His Lys Arg Glu Glu
 305 310 315 320

Phe Thr Asn Ala Glu Val Ala Phe
 325

<210> 12
 <211> 1352
 <212> DNA
 <213> Hordeum vulgare

<400> 12
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 aacaaggagg ttgatgcctt ggtccagaag atcaccggcc tccacccgc catcgccaag 120
 ctgcgtccctt tcagcccatc acccgacgtc gacgcgtct tcaccgcacct ggtcaccgcg 180
 tgcgtccccc cgagccccgt ggacgtgacc aagctcggtt cggaggcgca ggagatgcgg 240
 gagggcctca tcgcgcctcg ctccgaggcc gagggggaaagc tggaggcgca ctactccgac 300
 atgctggccg cttcgaccaa cccgctcgac cacccctggca tggatccctca ctacagcaac 360
 tacatcaacc tcagcaagct ggagtacgag ctccctggccg cgtacgtgcc gggcggcattc 420
 gccccggcccg ctgtcgcggtt catcgctcc ggcccgtgc cgttcagctc ctacgtccctc 480
 gccgctcgcc acctgcccga cgccatgttc gacaactacg acctgtgttag cgcggccaac 540
 gaccgtgcga gcaagctgtt ccgcgcggac aaggacgtgg gcccgcgtt gtctttccac 600
 accgcggacg tagcggaccc taccggcgag ctgcggcggt acgacgttgtt cttcctggcc 660
 ggcgtcgtgg gcatggctgc cgaggacaag gccaagggtga ttccgcacct cggcgcgcac 720
 atggcggacg gggcggccctt cgtcgcgcc agtgcgcagg cacgtgggtt cctctaccgg 780
 atcgtcgatc cccaggacat cggcgaggc gggtttgagg tgctggccgt gtgtcaccgg 840
 gacgatgacg tggtaactc cgtcatcatc gcacacaagt ccaaggacgt gcatgccaat 900
 gaacgtccca acggggcgtgg tggacagtac cggggcgcgg taccgggtt cagccgcgg 960
 tgcagggtcg gtgagatgtt ggcggacgtc acccacaaga gagaggagtt caccaacgcg 1020
 gaagtggcct tctgatcggtt gcgaggaaat gaaaatgaag gtggacgtgt gtggtcagca 1080
 tccatacggtt gctgcctgtt tcacgcgtt caatcgactt actacacttac tatgcagttc 1140
 aagtcatgtt ttgtcaatgtt aagtgtgtt tttacacttac tctatgaaag gcagggcaga 1200
 cgagggtagt gtgccaagttt acagtgtgtt attatagggtt taagtgttga gaataagacc 1260
 atttttgttc acaaatacgatc tgatgtatc ggtgtcatat tcgtattttagt tacatttgc 1320
 aagttgggtt ctaaaaaaaa aaaaaaaaaa aa 1352

<210> 13
 <211> 329
 <212> PRT
 <213> Hordeum vulgare

<400> 13
 Met Asp Ala Gln Ser Lys Glu Val Asp Ala Leu Val Gln Lys Ile Thr
 1 5 10 15

Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro Ser Pro
 20 25 30

Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys Val Pro Pro
 35 40 45

Ser Pro Val Asp Val Thr Lys Leu Ala Pro Glu Ala Gln Ala Met Arg
 50 55 60

Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu Glu Ala
 65 70 75 80

His Tyr Ser Asp Met Leu Ala Ala Phe Asp Asn Pro Leu Asp His Leu
 85 90 95

Gly Val Phe Pro Tyr Tyr Ser Asn Tyr Ile Asn Leu Ser Lys Leu Glu
 100 105 110

Tyr Glu Leu Leu Ala Arg Tyr Val Pro Gly Gly Ile Ala Pro Ala Arg
 115 120 125

Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Tyr Val Leu
 130 135 140

Ala Ala Arg His Leu Pro Asp Thr Val Phe Asp Asn Tyr Val Pro Val
 145 150 155 160

Arg Ala Ala Asn Asp Arg Ala Thr Arg Leu Phe Arg Ala Asp Lys Asp
 165 170 175

Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr
 180 185 190

Asp Glu Leu Ala Thr Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly
 195 200 205

Met Ala Ala Glu Asp Lys Gly Gln Gly Asp Pro His Leu Gly Ala His
 210 215 220

Met Ala Asp Gly Ala Ala Leu Val Arg Ser Ala His Gly Ala Arg Gly
 225 230 235 240

Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly Phe
 245 250 255

Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn Ser Val
 260 265 270

Ile Ile Ala Gln Lys Ser Lys Asp Met Phe Ala Asn Gly Pro Arg Asn
275 280 285

Gly Cys Gly Gly Arg Tyr Ala Arg Gly Thr Val Pro Val Val Ser Pro
290 295 300

Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val Thr Gln Lys Arg Glu
 305 310 315 320

Glu Phe Ala Lys Ala Glu Val Ala Phe
325

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<210> 14
<211> 1371
<212> DNA
<213> Hordeum vulgare
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<220>
<221> modified_base
<222> (8)
<223> a, c, g, t, unknown or other
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<400> 14
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tccagaagat caccggcctc cacggcccca tcgccaagct gccctcgctc agcccgccc 180
cgacgtcga cgcgtcttc accgacctgg tcacccgtg cgtgccccg agccccgtgg 240
acgtgaccaa gtcgccccg gaggcgagg cgatgcggg gggctcatac cgctctgtct 300
ccgaggccga gggcaagctg gaggcgact actccgacat gtcgccc ttcgacaacc 360
cgctcgacca ctcggcgctc ttccccact acagcaacta catcaacctc agcaagctcg 420
agtacgagct ctcggcgccg tacgtgccc gcgcatcgc cccggccccgc gtgcctca 480
tcggctccgg cccgctcccg ttcaagctct acgtcctcgc cgcgcggccac ctgcccgaca 540
ccgtgttcga caactacgtt cctgtgcgcg cggccaaacgca cgcgcgcgacc aggctgttcc 600
gchgaccaa ggacgtcgcc gcccgcattt cgttccacac cgcgcacgtc ggggaccta 660
ccgacgagct cgatcgatc gacgtcgctt tctggccgc gtcgtggc atggccgccc 720
aggacaaggg ccaagggtat ccgcacccgg gcgcgacat ggcggacggg gggccctcg 780
tccgcagcgc gcacggggcg cgtgggttcc tctaccggat cgtcgatccc caagacattt 840
gtcgaggcg gttcgagggtt ctgcgggtt gtcaccccgaa cgacgacgtg gtgaactccg 900
tcatcatcgc gcagaaggctt aaggacatgt ttggcaatgg acctcgcaac ggggtgtgtt 960
gacggtaatgc gcgaggcacg gtgcgggtgg tcagcccgcc ctgcaggatc ggcgagatgg 1020
tggcagacgt gacccagaag agagaggagt ttggcaaggc ggaagtggcc ttctgattgc 1080
tgcgaggctca ccatccgtat gccgcgtcta ccttcaata tcttgcaatc gtaggtggcg 1140
atttccatc tcttgttacg acctttcaaa tcatatgttg tttgtaccca ataatgtt 1200
tgtgttgc ttacacgcgcgt gtcttgtaca ctcggctctt agaaggcagg gcagatcaag 1260
agactgtgca aaggaaaaaga aatgtgtt gtttaggtt tatgagttgg gagaagatgt 1320
attctatgttcc aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa a 1371

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<210> 15
<211> 324
<212> PRT
<213> *Oryza sativa*

<400> 15
Met Glu Ala Gln Asn Gln Glu Val Ala Ala Leu Val Glu Lys Ala Gly
1 5 10 15

Leu His Ala Ala Ser Lys Leu Pro Ser Leu Ser Pro Ser Ala Glu Val
 20 25 30

Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys Val Pro Ala Ser Pro
 35 40 45

Val Asp Val Ala Lys Leu Gly Pro Glu Ala Gln Ala Met Arg Glu Glu
 50 55 60

Leu Arg Leu Cys Ser Ala Ala Glu Gly His Leu Glu Ala His Tyr Ala
 65 70 75 80

Asp Met Leu Ala Ala Phe Asp Asn Pro Leu Asp His Leu Ala Arg Phe
 85 90 95

Pro Tyr Tyr Gly Asn Tyr Val Asn Leu Ser Lys Leu Glu Tyr Asp Leu
 100 105 110

Leu Val Arg Tyr Val Pro Gly Ala Pro Thr Arg Val Ala Phe Val Gly
 115 120 125

Ser Gly Pro Leu Pro Phe Ser Ser Leu Val Leu Ala Ala His His Leu
 130 135 140

Pro Asp Ala Val Phe Asp Asn Tyr Asp Arg Cys Gly Ala Ala Asn Glu
 145 150 155 160

Arg Ala Arg Arg Leu Phe Arg Gly Ala Asp Glu Gly Leu Gly Ala Arg
 165 170 175

Met Ala Phe His Thr Ala Asp Val Ala Thr Leu Thr Gly Glu Leu Gly
 180 185 190

Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala Ala Glu
 195 200 205

Glu Lys Ala Gly Val Ala His Leu Gly Ala His Met Ala Asp Gly Ala
 210 215 220

Ala Leu Val Val Arg Thr Ala His Gly Ala Arg Gly Phe Leu Tyr Pro
 225 230 235 240

Val Asp Pro Glu Asp Val Arg Arg Gly Gly Phe Asp Val Leu Ala Val
 245 250 255

Cys His Pro Glu Asp Glu Val Asn Ser Val Val Ala Arg Lys Val Gly
 260 265 270

Ala Ala Ala Ala Ala Ala Ala Arg Arg Asp Glu Leu Ala Asp Ser
 275 280 285

Arg Gly Val Val Leu Pro Val Val Gly Pro Pro Ser Thr Cys Cys Lys
 290 295 300

Val Glu Ala Ser Ala Val Glu Lys Ala Glu Glu Phe Ala Ala Asn Lys
 305 310 315 320

Glu Leu Ser Val

<210> 16
 <211> 1372
 <212> DNA
 <213> Oryza sativa

<400> 16
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 cgtgttccca accgcgacaa agttcacag atggaggctc agaacaaga ggtcgctgcc 120
 ctggtcgaga agatcgccgg cctccacgcc gccatctcca agctccgctc gctgagccca 180
 tccgcccagg tggacgcgct cttcaccgc ctcgtcacgg cgtgcgtccc ggcgagcccc 240
 gtcgacgtgg ccaagctcg cccggaggcg caggcgatgc gggaggagct catccgcctc 300
 tgctcgccg ccgaggggcca ctcgaggcg cactacgccc acatgctcgc cgccttcgac 360
 aaccgcgtcg accacctcg cgcgtcccg tactacggca actacgtcaa cctgagcaag 420
 ctggagtagc acctcctcg cgcgtacgtc cccggcattt ccccccacccg cgtcgcccttc 480
 gtcgggtcgg gcccgtgcc gttcagctcc ctcgtgcgtc ctgcgcacca ctcgcccggac 540
 gcggtgttcg acaactacga cgggtgcggc gggcccaacg agcggggcggag gagggtgttc 600
 cggggcggcc acgaggggctt cggcgcgcgc atggcgttcc acaccggcga cgtggcgacc 660
 ctgacggggg agctcgccgc gtacgacgtc gtgttctgg cggcgctcg gggcatggcg 720
 gcccaggaga aggccggggt gatcgccac ctgggcgcgc acatggcgga cggcgccggc 780
 ctcgtcgtgc ggacggcgcg cggggcgcgc gggttctgt acccgatcg tgcgtcccgag 840
 gacgtcaggc gtggcggtt cgcgttctg gcggtgtgcc acccgagga cgaggtgatc 900
 aactccgtca tcgtcgcccg caaggtcggt gcccgcgcg cggccgcgc ggcgcgcaga 960
 gacgagctcg cggactcgcc cggcgtggc ctgcccgtgg tcggggcgcc gtccacgtgc 1020
 tgcaaggtgg aggcgagcgc gttgagaag gcagaagagt ttgcgccaa caaggagctg 1080
 tccgtcta ac agccggacga tcgaaaaggcg cactatatta tggcaataaa tcatttattt 1140
 atacttatgc tgcatttgcg aagctaagg atactatgca agccatatgt ttgtgttcgt 1200
 acgtgttgg tggacgtac agttgttg ttgtacgtc tgaagtactg aagtgttac 1260
 agtagatcac aagttcacag caatcaatga ggaccctgtt agccagtgtt aacgaggaac 1320
 atgccatctg tggatgacag tgagaaatta tataagaaaa acattttgtt ac 1372

<210> 17
 <211> 320
 <212> PRT
 <213> Arabidopsis thaliana

<400> 17
 Met Ala Cys Gln Asn Asn Leu Val Val Lys Gln Ile Ile Asp Leu Tyr
 1 5 10 15

Asp Gln Ile Ser Lys Leu Lys Ser Leu Lys Pro Ser Lys Asn Val Asp
 20 25 30

Thr Leu Phe Gly Gln Leu Val Ser Thr Cys Leu Pro Thr Asp Thr Asn
 35 40 45

Ile Asp Val Thr Asn Met Cys Glu Glu Val Lys Asp Met Arg Ala Asn
 50 55 60

Leu Ile Lys Leu Cys Gly Glu Ala Glu Gly Tyr Leu Glu Gln His Phe
 65 70 75 80

Ser Thr Ile Leu Gly Ser Leu Gln Glu Asp Gln Asn Pro Leu Asp His
 85 90 95

Leu His Ile Phe Pro Tyr Tyr Ser Asn Tyr Leu Lys Leu Gly Lys Leu
 100 105 110

Glu Phe Asp Leu Leu Ser Gln His Ser Ser His Val Pro Thr Lys Ile
 115 120 125

Ala Phe Val Gly Ser Gly Pro Met Pro Leu Thr Ser Ile Val Leu Ala
 130 135 140

Lys Phe His Leu Pro Asn Thr Thr Phe His Asn Phe Asp Ile Asp Ser
 145 150 155 160

His Ala Asn Thr Leu Ala Ser Asn Leu Val Ser Arg Asp Pro Asp Leu
 165 170 175

Ser Lys Arg Met Ile Phe His Thr Thr Asp Val Leu Asn Ala Thr Glu
 180 185 190

Ala Leu Asp Gln Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met
 195 200 205

Asp Lys Glu Ser Lys Val Lys Ala Ile Glu His Leu Glu Lys His Met
 210 215 220

Ala Pro Gly Ala Val Leu Met Leu Arg Arg Ala His Ala Leu Arg Ala
 225 230 235 240

Phe Leu Tyr Pro Ile Val Asp Ser Ser Asp Leu Lys Gly Phe Gln Leu
 245 250 255

Leu Thr Ile Tyr His Pro Thr Asp Asp Val Val Asn Ser Val Val Ile
 260 265 270

Ala Arg Lys Leu Gly Gly Pro Thr Thr Pro Gly Val Asn Gly Thr Arg
 275 280 285

Gly Cys Met Phe Met Pro Cys Asn Cys Ser Lys Ile His Ala Ile Met
 290 295 300

Asn Asn Arg Gly Lys Lys Asn Met Ile Glu Glu Phe Ser Thr Ile Glu
 305 310 315 320

<210> 18

<211> 963

<212> DNA

<213> *Arabidopsis thaliana*

<400> 18

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 acgtgcttac ccacggatac aaacatcgat gtcacaata tgtgtgaaga agtcaaagac 180
 atgagagcta atctcatcaa gctttgtggt gaagccgaag gttatggta gcaacacttc 240
 tccacaattt tgggatcttt acaagaagac caaaaacccac ttgaccattt acacatctt 300
 ccttactact ccaactacct caagcttaggc aagctcgagt tcgatctcct gagccaacac 360
 tcaagccatg tccccaccaa gattgccttc gtgggttcgg gtccgatgcc ttcacatcc 420
 atcgtattgg ccaagttca cttcccaac acgacgttcc acaacttga catcgactca 480

cacgcaaaca	cactcgcttc	aaacacctgtc	tctcgcgacc	cgAACCTCTC	aaaacgcatt	540
atcttccaca	caacggacgt	actaaacgca	accgaagccc	ttgaccaata	tgacgtcggt	600
ttcttagcgg	cgcttgttagg	gatggacaaa	gagtcaaagg	tcaaagccat	cgagcacttg	660
gagaaacaca	tggctctgg	agctgttctt	atgctaagga	gggctcatgc	tctcagagct	720
ttcttataatc	caatcgttga	ctcgctgtat	ctcaaaggct	ttcaactctt	gaccatctat	780
catccaacccg	atgacgtggt	taactcggtt	gtgatcgac	gtaagctcggt	ttggccgacc	840
acgccccgggg	ttaatggtac	tcgtggatgc	atgtttatgc	cttgcactgt	ctccaagatt	900
cacgcgatca	tgaacaaccg	tggtaagaag	aatatgatcg	aggagtttag	taccatcgag	960
taa						963

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<210> 19
<211> 320
<212> PRT
<213> Arabidopsis thaliana

<400> 19
Met Ala Cys Gln Asn Asn Leu Val Val Lys Gln Ile Met Asp Leu Tyr
1 5 10 15

Asn Gln Ile Ser Asn Leu Glu Ser Leu Lys Pro Ser Lys Asn Val Asp
20 25 30

Thr Leu Phe Arg Gln Leu Val Ser Thr Cys Leu Pro Thr Asp Thr Asn
35 40 45

Ile Asp Val Thr Glu Ile His Asp Glu Lys Val Lys Asp Met Arg Ser
50 55 60

His Leu Ile Lys Leu Cys Gly Glu Ala Glu Gly Tyr Leu Glu Gln His
65 70 75 80

Phe Ser Ala Ile Leu Gly Ser Phe Glu Asp Asn Pro Leu Asn His Leu
85 90 95

His Ile Phe Pro Tyr Tyr Asn Asn Tyr Leu Lys Leu Gly Lys Leu Glu
100 105 110

Phe Asp Leu Leu Ser Gln His Thr Thr His Val Pro Thr Lys Val Ala
115 120 125

Phe Ile Gly Ser Gly Pro Met Pro Leu Thr Ser Ile Val Leu Ala Lys
130 135 140

Phe His Leu Pro Asn Thr Thr Phe His Asn Phe Asp Ile Asp Ser His
145 150 155 160

Ala Asn Thr Leu Ala Ser Asn Leu Val Ser Arg Asp Ser Asp Leu Ser
165 170 175

Lys Arg Met Ile Phe His Thr Thr Asp Val Leu Asn Ala Lys Glu Gly
180 185 190

Leu Asp Gln Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asp
195 200 205

Lys Glu Ser Lys Val Lys Ala Ile Glu His Leu Glu Lys His Met Ala
210 215 220

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Pro Gly Ala Val Val Met Leu Arg Ser Ala His Gly Leu Arg Ala Phe
 225 230 235 240
 Leu Tyr Pro Ile Val Asp Ser Cys Asp Leu Lys Gly Phe Glu Val Leu
 245 250 255
 Thr Ile Tyr His Pro Ser Asp Asp Val Val Asn Ser Val Val Ile Ala
 260 265 270
 Arg Lys Leu Gly Gly Ser Asn Gly Ala Arg Gly Ser Gln Ile Gly Arg
 275 280 285
 Cys Val Val Met Pro Cys Asn Cys Ser Lys Val His Ala Ile Leu Asn
 290 295 300
 Asn Arg Gly Met Glu Lys Asn Leu Ile Glu Glu Phe Ser Ala Ile Glu
 305 310 315 320

<210> 20
 <211> 963
 <212> DNA
 <213> Arabidopsis thaliana

<400> 20
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 aacctcgaga gcttaaaacc atccaagaat gtcgacactt tgttcagaca acttgtgtcc 120
 acgtgcttac caacggacac gaacatcgat gtcacagaga tacacatga aaaagtcaaa 180
 gacatgagat ctcatctcat caagcttgc ggtgaagccg aaggttattt agagcaacac 240
 ttttcagcaa tcttaggctc ttttgaagac aaccctctaa accatttaca catcttcccc 300
 tattacaaca actatctcaa actaggcaaa ctcgaattcg atctccttcc tcagcacaca 360
 acccatgtcc cgaccaaagt cgccatttatt ggttccggtc cgatgccact tacttccatc 420
 gtcttgccca agttccaccc ccccaacaca acgttccaca acttcgacat cgactcacac 480
 gccaacacac tcgcttcaaa cctcggttct cgtgattctg accttccaa acgcattgatt 540
 ttccacacaa ctgatgtatt aaacgctaag gaggggttag accaatacga tggtgtttc 600
 ttggcagctc ttgttggat ggataaaagag tcaaagggtca aagctattga gcatttagag 660
 aagcatatgg cccctggagg tgggttgatg ctaagaagggtc ctcattgtct tagagctttc 720
 ttgtatccaa tcggtgactc ttgtgatctt aaagggtttt aggtgttaac catttatcat 780
 ccgtctgacg acgtggtaa ttgggtgtc atcgacgta agctgggtgg tccaaatgg 840
 gctcgaggca gccagatcg 5 acgggtgtgt gttatgcctt gtaattgctc taagggtccac 900
 gcgatcttga acaatcgtgg tatggagaag aatttgcgtt agagggttag tgccatcgag 960
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<210> 21
 <211> 320
 <212> PRT
 <213> Arabidopsis thaliana

<400> 21
 Met Gly Cys Gln Asp Glu Gln Leu Val Gln Thr Ile Cys Asp Leu Tyr
 1 5 10 15
 Glu Lys Ile Ser Lys Leu Glu Ser Leu Lys Pro Ser Glu Asp Val Asn
 20 25 30

Ile Leu Phe Lys Gln Leu Val Ser Thr Cys Ile Pro Pro Asn Pro Asn
 35 40 45

Ile Asp Val Thr Lys Met Cys Asp Arg Val Gln Glu Ile Arg Leu Asn
 50 55 60

Leu Ile Lys Ile Cys Gly Leu Ala Glu Gly His Leu Glu Asn His Phe
 65 70 75 80

Ser Ser Ile Leu Thr Ser Tyr Gln Asp Asn Pro Leu His His Leu Asn
 85 90 95

Ile Phe Pro Tyr Tyr Asn Asn Tyr Leu Lys Leu Gly Lys Leu Glu Phe
 100 105 110

Asp Leu Leu Glu Gln Asn Leu Asn Gly Phe Val Pro Lys Ser Val Ala
 115 120 125

Phe Ile Gly Ser Gly Pro Leu Pro Leu Thr Ser Ile Val Leu Ala Ser
 130 135 140

Phe His Leu Lys Asp Thr Ile Phe His Asn Phe Asp Ile Asp Pro Ser
 145 150 155 160

Ala Asn Ser Leu Ala Ser Leu Leu Val Ser Ser Asp Pro Asp Ile Ser
 165 170 175

Gln Arg Met Phe Phe His Thr Val Asp Ile Met Asp Val Thr Glu Ser
 180 185 190

Leu Lys Ser Phe Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asn
 195 200 205

Lys Glu Glu Lys Val Lys Val Ile Glu His Leu Gln Lys His Met Ala
 210 215 220

Pro Gly Ala Val Leu Met Leu Arg Ser Ala His Gly Pro Arg Ala Phe
 225 230 235 240

Leu Tyr Pro Ile Val Glu Pro Cys Asp Leu Gln Gly Phe Glu Val Leu
 245 250 255

Ser Ile Tyr His Pro Thr Asp Asp Val Ile Asn Ser Val Val Ile Ser
 260 265 270

Lys Lys His Pro Val Val Ser Ile Gly Asn Val Gly Gly Pro Asn Ser
 275 280 285

Cys Leu Leu Lys Pro Cys Asn Cys Ser Lys Thr His Ala Lys Met Asn
 290 295 300

Lys Asn Met Met Ile Glu Glu Phe Gly Ala Arg Glu Glu Gln Leu Ser
 305 310 315 320

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<210> 22
<211> 963
<212> DNA
<213> Arabidopsis thaliana

<400> 22
atgggttgcc aagacgaaca attggtgcaa acaatatgcg atctctacga aaagatctca 60
aagcttgaga gtctaaaacc atccgaagat gtcaacattc tcttcaagca gtcgttcc 120
acatgcatac caccaaaccc taacatcgat gtcaccaaga tgtgtgacag agtccaagag 180
attcgactta atctcatcaa gatttgttgt cttagccaa gtcacttaga aaaccattc 240
tcttcgatct tgacctctta ccaagacaac ccacttcattc atttaaacat tttcccttat 300
tacaacaact attgaaaact cgaaaaagctc gagttcgacc tcctcgaaca aaacctaaat 360
ggctttgtcc caaagagtgt ggcttcatt ggatctggtc ctcttcctc cacttccatc 420
gttcttgctt cattccatct caaagacaca atcttcaca actttgacat cgacccatca 480
gcgaactcac tcgcttcctc tctgggttcc tctgatccag acatctctca acgcattgttc 540
ttccacaccc ttgtatataat ggacgtgaca gagagcttaa agagcttga tgcgtgtt 600
ctagctgctc ttgttggaaat gaacaaagag gagaaagtta aagtgatcga gcatctgcag 660
aaacacatgg ctcttgggtgc tgcgtcatg cttaggatgt ctcatggtcc gagagcggtt 720
ctttatccga tcggttgagcc tgcgtatctt caggggttcg aggtttgtc tatttatacac 780
ccaaacagatg atgttatcaa ctccgtggtg atctctaaaa agcatccagt tgcgtgtt 840
ggaaatgttg gtggcctaa ttcatgttttgc ctcaaggcctt gcaactgttc caagacccac 900
gcgaaaatga acaagaacat gatgatcgag gagttcgag ctagggagga acagttgtct 960
taa 963

<210> 23
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      consensus sequence

<220>
<221> MOD_RES
<222> (3)
<223> Variable amino acid residue

<220>
<221> MOD_RES
<222> (9)
<223> Variable amino acid residue

<220>
<221> MOD_RES
<222> (16)
<223> Variable amino acid residue

<220>
<221> MOD_RES
<222> (19)
<223> Variable amino acid residue

<220>
<221> MOD_RES
<222> (24)
<223> Variable amino acid residue

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<400> 23
Leu Pro Xaa Leu Ser Pro Ser Pro Xaa Val Asp Arg Leu Phe Thr Xaa
1 5 10 15

Leu Val Xaa Ala Cys Val Pro Xaa Ser Pro Val Asp Val Thr Lys Leu
20 25 30

<210> 24
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
consensus sequence

<220>
<221> MOD_RES
<222> (7)
<223> Variable amino acid residue

<220>
<221> MOD_RES
<222> (11)
<223> Variable amino acid residue

<400> 24
Leu Ile Arg Leu Cys Ser Xaa Ala Glu Gly Xaa Leu Glu Ala His Tyr
1 5 10 15

<210> 25
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
consensus sequence

<220>
<221> MOD_RES
<222> (7)
<223> Variable amino acid residue

<400> 25
Pro Leu Asp His Leu Gly Xaa Phe Pro Tyr
1 5 10

<210> 26
<211> 13
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      consensus sequence

<220>
<221> MOD_RES
<222> (4)
<223> Variable amino acid residue

<400> 26
Val Ala Phe Xaa Gly Ser Gly Pro Leu Pro Phe Ser Ser
      1           5           10

<210> 27
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      consensus sequence

<400> 27
Asp Val Val Phe Leu Ala Ala Leu Val Gly Met
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Xaa Xaa Xaa Xaa Xaa Leu Phe Xaa Xaa Leu Val Xaa Xaa Cys Xaa Pro Xaa
35 40 45

Xaa Xaa Xaa Asp Val Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Met Arg
50 55 60

Xaa Xaa Leu Ile Xaa Xaa Cys Xaa Xaa Ala Glu Xaa Xaa Leu Glu Xaa
65 70 75 80

His Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Asp Xaa Pro Leu Xaa His Leu
85 90 95

Xaa Xaa Phe Pro Tyr Xaa Xaa Asn Tyr Xaa Xaa Leu Xaa Xaa Leu Glu
100 105 110

Xaa Xaa Leu Leu Xaa Xaa
115 120 125

Ala Phe Xaa Gly Ser Gly Pro Leu Pro Xaa Xaa Ser Xaa Xaa Leu Ala
130 135 140

Xaa Xaa His Leu Xaa Xaa Xaa Xaa Phe Xaa Asn Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Xaa Ala Asn Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Leu Xaa Xaa Xaa Asp Val Val Phe Leu Ala Ala Xaa Val Gly
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Met Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa His Leu Xaa Xaa His
 210 215 220

Met Xaa Xaa Gly Ala Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
 225 230 235 240

Phe Leu Tyr Pro Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe
 245 250 255

Xaa Val Leu Xaa Val Xaa His Pro Xaa Xaa Xaa Val Xaa Asn Ser Xaa
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Xaa
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Xaa
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Xaa
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Ile Gln Ala

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 20 25 30
 Glu Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys Val Pro Ala
 35 40 45
 Ser Pro Val Asp Val Ala Lys Leu Gly Pro Glu Ala Gln Ala Met Arg
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 Glu Glu Leu Ile Arg Leu Cys
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 Pro Gly Ile Ala Pro Thr Arg Val Ala Phe Val Gly Ser Gly Pro Leu
 20 25 30
 Pro Phe Ser Ser Leu Val Leu Ala Ala His His Leu Pro Asp Ala Val
 35 40 45
 Phe Asp Asn Tyr Asp Arg Cys Gly Ala Ala Asn Glu Arg Ala Arg Arg
 50 55 60
 Leu Phe Arg Gly Ala Asp Glu Gly Leu Gly Ala Arg Met Ala Phe His
 65 70 75 80
 Thr Gly Asp Val Ala Thr Leu Thr Gly Glu Leu Gly Ala Tyr Asp Val
 85 90 95
 Val Phe Leu Ala Thr Leu Val Gly Met Ala Ala Glu Glu Lys Pro
 100 105 110

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 Tyr Asp Val Val Phe Leu Ala Ala Leu Val Asp Met Ala Ala Glu Glu
 20 25 30

Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met Val Glu Gly Ala
35 40 45

Ser Leu Val Val Tyr Ser Ala His Gly Ala Arg Gly Phe Leu Tyr Pro
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Tyr Asp Val

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